

#6

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/809,638

DATE: 08/08/2001
TIME: 11:01:34

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\08082001\I809638.raw

```

4 <110> APPLICANT: Mary Faris
5   Pia M. Challita-Eid
6   Steve Chappell Mitchell
7   Daniel E.H. Afar
8   Arthur B. Raitano
9   Aya Jakobovits
11 <120> TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN
12   HIGHLY EXPRESSED IN VARIOUS CANCERS
15 <130> FILE REFERENCE: 129.35US01
17 <140> CURRENT APPLICATION NUMBER: 09/809,638
18 <141> CURRENT FILING DATE: 2001-03-14
20 <160> NUMBER OF SEQ ID NOS: 746
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2103
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1

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32 gggcttgaag gtttttagtat agcatttctt tctccaatat tcctaacaat tactccccc	180
33 tggaaattgg ttaacaagaa gtggatgcta accctgctga ggataatcac tattggcage	240
34 atagcctcct tccaggctcc aaatgcacaa cttcgactga tggttcttgc gcttgggtg	300
35 tcttcctcac tgatagtgcg agctgtgact tgggtgtcgg gaagtcatgg ccaaaggta	360
36 ctcagaattt gggattcat tttaggacag attgttcttgc ttgttctacg catatggat	420
37 acttcactaa acccaatctg gagttatca gatgtccaaaca aagtgtataact gacattaagt	480
38 gccatagcca cacttgcgtc tattggcaca gatgggtact gcagtaaaacc tgaagaaaag	540
39 aagactggtg aggttagccac ggggatggcc tctagacccaa actggctgtc ggcagggct	600
40 gctttggta gccttgcgtt ctcacccac tgggtttttg gagaagtctc tcttgggtcc	660
41 agatgggcag tgagtggca tccacatcca gggccagatc ctaacccatt tggaggtgca	720
42 gtactgctgt gcttggcaag tgattgtat cttccatctt gtttgggtt tcgtgtact	780
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45 acacttggac accttattaa ctcaggacaa aaccctggaa aaaccatgac cattgccatg	960
46 atattttata ttctagaaat attttctgt gcctggcgtc cagttttaa gtttggccca	1020
47 ggaggtgtct acgctagaga aagatcagat gtgctttgg ggacaatgtat gttattatc	1080
48 gggctgaata tgctattgg tcctaagaaa aacctgtact tgcttcttc aacaaaaaac	1140
49 agttctaaag tgctttcag aaagagtggaa aaatacatga aactttttct gtggctgtct	1200
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51 aaagtggcac caaccaaaga ggtctctgc gccatctggc ctttcaggtt tggatatgac	1320
52 aatgaagggt ggtcttagtct agaaagatca gtcacactgc tcaatgaaac aggtgcagat	1380
53 ttcataacaa ttttggagag tgatgtttctt aagccctata tggggaaacaa tgacttaacc	1440
54 atgtggctag gggaaaagtt ggtttctat acagactttg gtccaaagcac aaggatcac	1500
55 actggggga ttatggcttt gtcagatc ccaattgtga aatctgagca tcacccctt	1560
56 ccgtcaccag agggcgagat cgaccacgac atcacattga cctttaacat ttcggcaag	1620
57 ctgggtggatt ttgtcgtgac acactttggg aaccacgaaag atgacctcga cagggaaactg	1680
58 caggctattt ctgtttcaaa actactgaaa agtagctcta atcaagtgtat atttctggga	1740

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59	tatatactt	cagcacctgg	ctccagagat	tatctacagc	tcactgaaca	tggcaatgtg	1800									
60	aaggatatcg	acagcaactga	tcatgacaga	tggtgtgaat	acattatgtt	tcgagggctg	1860									
61	atcaggttgg	gttatcaag	aatctccat	gctgaactga	gtgattcaga	aattcagatg	1920									
62	gc当地attn	ggatccctga	tgaccccact	aattatacg	acaaccagaa	agtggtcata	1980									
63	gaccacagag	aagtttctga	gaaaattcat	tttaatccca	gatttggatc	ctacaaagaa	2040									
64	ggacacaatt	atgaaaacaa	ccatcatttt	catatgaata	ctcccaaata	cttttatga	2100									
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67	<210>	SEQ ID NO:	2													
68	<211>	LENGTH:	699													
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70	<213>	ORGANISM:	Homo sapiens													
72	<400>	SEQUENCE:	2													
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74	1							5				10				15
75	Val	Ser	Trp	Ser	Leu	Tyr	His	Asp	Leu	Gly	Pro	Met	Ile	Tyr	Tyr	Phe
76								20				25				30
77	Pro	Leu	Gln	Thr	Leu	Glu	Leu	Thr	Gly	Leu	Glu	Gly	Phe	Ser	Ile	Ala
78								35				40				45
79	Phe	Leu	Ser	Pro	Ile	Phe	Leu	Thr	Ile	Thr	Pro	Phe	Trp	Lys	Leu	Val
80								50				55				60
81	Asn	Lys	Lys	Trp	Met	Leu	Thr	Leu	Leu	Arg	Ile	Ile	Thr	Ile	Gly	Ser
82	65							70				75				80
83	Ile	Ala	Ser	Phe	Gln	Ala	Pro	Asn	Ala	Lys	Leu	Arg	Leu	Met	Val	Leu
84								85				90				95
85	Ala	Leu	Gly	Val	Ser	Ser	Ser	Leu	Ile	Val	Gln	Ala	Val	Thr	Trp	Trp
86								100				105				110
87	Ser	Gly	Ser	His	Leu	Gln	Arg	Tyr	Leu	Arg	Ile	Trp	Gly	Phe	Ile	Leu
88								115				120				125
89	Gly	Gln	Ile	Val	Leu	Val	Val	Leu	Arg	Ile	Trp	Tyr	Thr	Ser	Leu	Asn
90								130				135				140
91	Pro	Ile	Trp	Ser	Tyr	Gln	Met	Ser	Asn	Lys	Val	Ile	Leu	Thr	Leu	Ser
92	145							145				150				160
93	Ala	Ile	Ala	Thr	Leu	Asp	Arg	Ile	Gly	Thr	Asp	Gly	Asp	Cys	Ser	Lys
94								165				170				175
95	Pro	Glu	Glu	Lys	Lys	Thr	Gly	Glu	Val	Ala	Thr	Gly	Met	Ala	Ser	Arg
96								180				185				190
97	Pro	Asn	Trp	Leu	Leu	Ala	Gly	Ala	Ala	Phe	Gly	Ser	Leu	Val	Phe	Leu
98								195				200				205
99	Thr	His	Trp	Val	Phe	Gly	Glu	Val	Ser	Leu	Val	Ser	Arg	Trp	Ala	Val
100								210				215				220
101	Ser	Gly	His	Pro	His	Pro	Gly	Pro	Asp	Pro	Asn	Pro	Phe	Gly	Ala	
102	225							225				230				240
103	Val	Leu	Leu	Cys	Leu	Ala	Ser	Gly	Leu	Met	Leu	Pro	Ser	Cys	Leu	Trp
104								245				250				255
105	Phe	Arg	Gly	Thr	Gly	Leu	Ile	Trp	Trp	Val	Thr	Gly	Thr	Ala	Ser	Ala
106								260				265				270
107	Ala	Gly	Leu	Leu	Tyr	Leu	His	Thr	Trp	Ala	Ala	Ala	Val	Ser	Gly	Cys
108								275				280				285
109	Val	Phe	Ala	Ile	Phe	Thr	Ala	Ser	Met	Trp	Pro	Gln	Thr	Leu	Gly	His

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110	290	295	300
111	Leu Ile Asn Ser Gly Thr Asn Pro Gly Lys Thr Met Thr Ile Ala Met		
112	305	310	315
113	Ile Phe Tyr Leu Leu Glu Ile Phe Phe Cys Ala Trp Cys Thr Ala Phe		320
114	325	330	335
115	Lys Phe Val Pro Gly Gly Val Tyr Ala Arg Glu Arg Ser Asp Val Leu		
116	340	345	350
117	Leu Gly Thr Met Met Leu Ile Ile Gly Leu Asn Met Leu Phe Gly Pro		
118	355	360	365
119	Lys Lys Asn Leu Asp Leu Leu Leu Gln Thr Lys Asn Ser Ser Lys Val		
120	370	375	380
121	Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu		
122	385	390	395
123	400	405	410
124	Val Gly Val Gly Leu Leu Gly Leu Gly Leu Arg His Lys Ala Tyr Glu		415
125	Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile		
126	420	425	430
127	Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu		
128	435	440	445
129	Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile		
130	450	455	460
131	Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr		
132	465	470	475
133	480	485	490
134	495	500	505
135	510	515	520
136	525	530	535
137	540	545	550
138	555	560	565
139	570	575	580
140	585	590	595
141	600	605	610
142	615	620	625
143	630	635	640
144	645	650	655
145	660	665	670
146	675	680	685

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159	His	Phe	His	Met	Asn	Thr	Pro	Lys	Tyr	Phe	Leu					
160	690						695									
162	<210>	SEQ ID NO:	3									60				
163	<211>	LENGTH:	287									120				
164	<212>	TYPE:	DNA									180				
165	<213>	ORGANISM:	Homo sapiens									240				
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169	gaggcagggt	ctgaagtgtat	atatcccaga	aatatcaactt	gatttagagct	acttttcagt										
170	agttttgaaa	cagcaatacg	ctgcagtttc	ctgtcgaggt	catcttcgtg	gttcccaaag										
171	tgtgtcacga	caaaatccac	cagttgccc	gaaatgttaa	cggtcaatgt	gatggcttgt										
172	gcatcttgc	tgtgtggcc	aggctggct	caacgtgcag	atagatc											
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175	<211>	LENGTH:	699													
176	<212>	TYPE:	PRT													
177	<213>	ORGANISM:	Homo sapiens													
179	<400>	SEQUENCE:	4													
180	Met	Thr	Ser	Leu	Trp	Arg	Glu	Ile	Leu	Glu	Ser	Leu	Leu	Gly	Cys	
181	1			5				10				15				
182	Val	Ser	Trp	Ser	Leu	Tyr	His	Asp	Leu	Gly	Pro	Met	Ile	Tyr	Tyr	Phe
183					20				25				30			
184	Pro	Leu	Gln	Thr	Leu	Glu	Leu	Thr	Gly	Leu	Glu	Gly	Phe	Ser	Ile	Ala
185					35				40			45				
186	Phe	Leu	Ser	Pro	Ile	Phe	Leu	Thr	Ile	Thr	Pro	Phe	Trp	Lys	Leu	Val
187					50				55			60				
188	Asn	Lys	Lys	Trp	Met	Leu	Thr	Leu	Leu	Arg	Ile	Ile	Thr	Ile	Gly	Ser
189		65				70				75			80			
190	Ile	Ala	Ser	Phe	Gln	Ala	Pro	Asn	Ala	Lys	Leu	Arg	Leu	Met	Val	Leu
191					85				90			95				
192	Ala	Leu	Gly	Val	Ser	Ser	Ser	Leu	Ile	Val	Gln	Ala	Val	Thr	Trp	Trp
193					100				105			110				
194	Ser	Gly	Ser	His	Leu	Gln	Arg	Tyr	Leu	Arg	Ile	Trp	Gly	Phe	Ile	Leu
195					115				120			125				
196	Gly	Gln	Ile	Val	Leu	Val	Val	Leu	Arg	Ile	Trp	Tyr	Thr	Ser	Leu	Asn
197					130				135			140				
198	Pro	Ile	Trp	Ser	Tyr	Gln	Met	Ser	Asn	Lys	Val	Ile	Leu	Thr	Leu	Ser
199		145				150				155			160			
200	Ala	Ile	Ala	Thr	Leu	Asp	Arg	Ile	Gly	Thr	Asp	Gly	Asp	Cys	Ser	Lys
201					165				170			175				
202	Pro	Glu	Glu	Lys	Lys	Thr	Gly	Glu	Val	Ala	Thr	Gly	Met	Ala	Ser	Arg
203					180				185			190				
204	Pro	Asn	Trp	Leu	Leu	Ala	Gly	Ala	Ala	Phe	Gly	Ser	Leu	Val	Phe	Leu
205					195				200			205				
206	Thr	His	Trp	Val	Phe	Gly	Glu	Val	Ser	Leu	Val	Ser	Arg	Trp	Ala	Val
207					210				215			220				
208	Ser	Gly	His	Pro	His	Pro	Gly	Pro	Asp	Pro	Asn	Pro	Phe	Gly	Gly	Ala
209		225				230				235			240			
210	Val	Leu	Leu	Cys	Leu	Ala	Ser	Gly	Leu	Met	Leu	Pro	Ser	Cys	Leu	Trp
211					245				250			255				

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212 Phe Arg Gly Thr Gly Leu Ile Trp Trp Val Thr Gly Thr Ala Ser Ala
 213 260 265 270
 214 Ala Gly Leu Leu Tyr Leu His Thr Trp Ala Ala Ala Val Ser Gly Cys
 215 275 280 285
 216 Val Phe Ala Ile Phe Thr Ala Ser Met Trp Pro Gln Thr Leu Gly His
 217 290 295 300
 218 Leu Ile Asn Ser Gly Thr Asn Pro Gly Lys Thr Met Thr Ile Ala Met
 219 305 310 315 320
 220 Ile Phe Tyr Leu Leu Glu Ile Phe Phe Cys Ala Trp Cys Thr Ala Phe
 221 325 330 335
 222 Lys Phe Val Pro Gly Gly Val Tyr Ala Arg Glu Arg Ser Asp Val Leu
 223 340 345 350
 224 Leu Gly Thr Met Met Leu Ile Ile Gly Leu Asn Met Leu Phe Gly Pro
 225 355 360 365
 226 Lys Lys Asn Leu Asp Leu Leu Gln Thr Lys Asn Ser Ser Lys Val
 227 370 375 380
 228 Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu
 229 385 390 395 400
 230 Val Gly Val Gly Leu Leu Gly Leu Gly Leu Arg His Lys Ala Tyr Glu
 231 405 410 415
 232 Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile
 233 420 425 430
 234 Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu
 235 435 440 445
 236 Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile
 237 450 455 460
 238 Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr
 239 465 470 475 480
 240 Met Trp Leu Gly Glu Lys Leu Gly Phe Tyr Thr Asp Phe Gly Pro Ser
 241 485 490 495
 242 Thr Arg Tyr His Thr Trp Gly Ile Met Ala Leu Ser Arg Tyr Pro Ile
 243 500 505 510
 244 Val Lys Ser Glu His His Leu Leu Pro Ser Pro Glu Gly Glu Ile Ala
 245 515 520 525
 246 Pro Ala Ile Thr Leu Thr Val Asn Ile Ser Gly Lys Leu Val Asp Phe
 247 530 535 540
 248 Val Val Thr His Phe Gly Asn His Glu Asp Asp Leu Asp Arg Lys Leu
 249 545 550 555 560
 250 Gln Ala Ile Ala Val Ser Lys Leu Leu Lys Ser Ser Ser Asn Gln Val
 251 565 570 575
 252 Ile Phe Leu Gly Tyr Ile Thr Ser Ala Pro Gly Ser Arg Asp Tyr Leu
 253 580 585 590
 254 Gln Leu Thr Glu His Gly Asn Val Lys Asp Ile Asp Ser Thr Asp His
 255 595 600 605
 256 Asp Arg Trp Cys Glu Tyr Ile Met Tyr Arg Gly Leu Ile Arg Leu Gly
 257 610 615 620
 258 Tyr Ala Arg Ile Ser His Ala Glu Leu Ser Asp Ser Glu Ile Gln Met
 259 625 630 635 640
 260 Ala Lys Phe Arg Ile Pro Asp Asp Pro Thr Asn Tyr Arg Asp Asn Gln

VERIFICATION SUMMARY

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